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ABSTRACT

Growth of microalgal-bacterial biomass on primary treated wastewater

S.J. Turner*[1], K. Biswas[1], J.M. Valigore[2] and A.D. O'Sullivan[2]

[1]School of Biological Sciences, The University of Auckland, PBag 92019 Auckland, NZ.
[2]Hydrological and Ecological Engineering Group, Department of Civil and Natural Resources Engineering, University of Canterbury, Christchurch, NZ.

The use of microalgae as an economically viable feedstock for biofuel production requires development of efficient methods for growth and harvest of biomass. Here we describe a preliminary investigation of the growth and settling characteristics of microalgal-bacterial biomass using primary treated wastewater from the Christchurch Wastewater Treatment Plant (CWTP) as a nutrient source. Sequencing batch reactors (SBRs) were established using a mixture of oxidation pond and primary treated wastewater from CWTP. Microalgal-bacterial flocs were developed by systematically discarding the non-settleable material (supernatant) and retaining settleable solids within the reactors. Subsequent addition of activated sludge (AS) improved the settleability of the biomass but resulted in development of anaerobic conditions and increased the ammonia, COD, and TSS concentrations in reactor supernatants. Analysis of 16S ribosomal RNA (rRNA) gene clone libraries prepared from settleable and suspended (supernatant) fractions revealed distinct differences in the bacterial community structure. Settled biomass was dominated by *Firmicutes* (45%) of which 80% were members of the Clostridia. *Proteobacteria* were also abundant (39%) and included, in order of dominance, the γ- (20%) β- (10%), and α- (8%) classes. In contrast, the supernatant community was dominated by β- *Proteobacteria* (60%) followed by Firmicutes (26%). Further studies are planned to verify these results and determine the possible bioflocculation role of *Proteobacteria* in this context.